

FIGURE 1

Rattus norvegicus laminin-5 alpha 3 chain
Contains G1 thru G5 subdomains
Cloned as SacI blunt/XbaI fragment

GAGCTCATTCGCAGGCCAGAGATGCTGCGAACAAAGGTTGCAATTCCCATGAGGTTCAATGGT
AAATCTGGTGTTGAAGTCCGTCTGCCAAATGACCTAGAAGACTTGAAGGGATACACGTCTCT
GTCTTTGTTCCCTCCAAAGACCAGACTTAAGAGAGAATGGAGGCACTGAGGACATGTTTGTA
TGTACCTTGGAACAAGGATGCCTCCAAGGACTACATCGGCATGGCGGTTGTAGATGGCCAG
CTGACGTGTGTCTACAACCTGGGGGACCGAGAAGCTGAAGTTCAGATCGATCAGGTCCTGAC
GGAGAGTGAGTCTCAGGAGGCAGTTATGGACCGGGTGAAGTTCAGAGAATATATCAATTTG
CCAAGCTTAATTACACCAAAGAAGCCACGTCCAATAAACCCAAAGCTCCCGCGGTCTACGAC
CTGGAGGGTGGCAGTAGCAACACGCTCCTTAATTTGGATCCCGAGGACGCTGTGTTTTATGT
CGGAGGTTACCCACCGGATTTTGAAGTTCCTAGCAGACTGCGGTTCCCTCCATACAAAGGCT
GTATCGAACTAGATGACCTCAATGAAAACGTTCTAAGCTTGTACAATTTCAAGACAACTTTC
AATCTCAACACCACGGAGGTGGAGCCTTGTAGGAGGAGAAAGGAAGAGTCAGACAAAAATTA
CTTTGAAGGTACAGGCTATGCTCGCATCCCTACTCAACCAAATGCTCCCTTCCCAAACCTCA
TACAGACCATCCAGACTACTGTGGACAGAGGTTTACTGTTCTTCGCAGAAAACCAGGATAAC
TTCATATCTCTGAACATAGAAGATGGCAATCTCATGGTGAGATACAACTAAATTCAGAGCC
ACCCAAAGAGAAGGGAATTCGAGACACCATCAACGATGGGAAAGATCATTGATCTTAATCA
CAATTGAAAACTACAAAAACGCATGTGGATAAATGTGAACGAACGCAGTGTACGAATCGAA
GGGGAATATTTGATTTTCAGCACATATTATTTGGGCGGAATTCCAATTGCAATCAGAGAAAG
GTTTAACATCTCAACGCCTGCTTTCCAAGGCTGCATGAAGAATCTGAAGAAAACCAGTGGGG
TTGTCAGGTTGAATGATACTGTGGGTGTAACCAAGAAGTGCTCAGAAGACTGGAAGCTTGTG
CGAACCGCCTCGTTCTCCAGAGGAGGGCAGATGAGCTTTACAACTTGGACGTGCCCTCGAC
TGACCGCTTCCAGCTCTCCTTTGGGTTTTCAGACCTTTCAACCCAGTGGCACACTGCTCAATC
ATCAGACGCGGACAAGCAGCCTGCTGGTCACCTGGAAGATGGGCACATTGAGTTGAGCACT
AGGGACAGCAACATCCCAATTTTCAAGTCTCCAGGGACCTACATGGACGGTTTACTGCATCA
TGTATCTGTAATAAGTGACACCTCAGGTCTCCGCCTTCTCATCGATGACCAGGTCTTGAGAA
GGAACCAGAGGCTTCTAGCTTCTCTAACGCCCCAGCAGTCGCTCCGCCTTGGAGGAGGTCAT
TTCGAGGGTTGTATCAGCAATGTTTTAGTCCAAAGGTTTTTCAGAGTCCAGAAGTCTTGGA
TCTGGCCAGTAAATCTACCAAGAAGGATGCATCCCTAGGAGGCTGCAGTTTAAACAAGCCAC
CTTTTCTTATGTTGTTTAAAAGTCCCAAGAGATTTAAACAAGGGCCGGATTTTCAATGTTAAT
CAGCTGATGCAAGATGCACCTCAGGCCACAAGGAGCACAGAGGCTTGGCAAGATGGGAGGTC
CTGCCTACCACCTCTGAACACCAAGGCCTCTCACAGAGCCCTGCAGTTTGGAGACAGCCCCA
CCAGCCACTTGCTACTCAAGCTTCCCCAGGAACTGCTGAAACCTAGGTCACAGTTTTCTTTA
GACATACAGACAACCTTCCCCCAAAGGACTGGTGTTTTACGCAGGCACCAAGGACTCCTTCCT
GGCTCTTTATGTGCGAGATGGCCGTGTTGTCTTTGCTTTGGGGGCAGGAGGGAAGAACTGA
GACTCAGGAGCAAGGAGAGATACCATGACGGGAAGTGGCACACGGTGGTGTTCGGAATAAT
GGAGGAAAGGCACGCCTGGTTGTGGATGGGCTAAGGGCCAGGAAGGCAGTTTGCCTGGAAA
TTCTACCATCAGCCCCAGAGAACAGGTTTACCTAGGGTTGCCGCTATCAAGAAAGCCAAAGA
GCCTACCCAGCACAGTTTTGTGGGGTGCTGAGAGATTTCCAGTTGAACTCGAAACCCCTG
GATTCTCCTTCTGCGAGGTTTGGGGTATCTCCCTGCTTGGGTGGCTCTTTAGAGAAAGGCAT
TTATTTCTCCCAAGGAGGAGGCCATGTGATCCTAGCCAATTCTGTGTCCTTGGGGCCAGAGC
TTAAGCTCACTTTCAGCATTCGCCCACGGAGTCTCACTGGGGTCTTAATACACGTCCGAAGT

**CAATCTGGACAGCGCTTAAGTGTGTACATGGAGGCAGGAAAGGTCACAACCTCTGTGAGCAG
TGATGCAGGAGGAAGTGTGACATCAATTACACCGAAGCAGTCTCTGTGTGATGGACAGTGGC
ACTCGGTGGCAGTCTCCATTAAACAGCGCATCCTGCATCTAGA**

48 atgaggttcaatggtaaactctggtggtgaagtcggtctgccaaat
M R F N G K S G V E V R L P N
93 gacctagaagacttgaagggatacacgtctctgtctttgttcctc
D L E D L K G Y T S L S L F L
138 caaagaccagacttaagagagaatggaggcactgaggacatgttt
Q R P D L R E N G G T E D M F
183 gtaatgtaccttggaaacaaggatgcctccaaggactacatcggc
V M Y L G N K D A S K D Y I G
228 atggcggtttagatggccagctgacgtgtgtctacaacctgggg
M A V V D G Q L T C V Y N L G
273 gaccgagaagctgaagttcagatcgatcaggtcctgacggagagt
D R E A E V Q I D Q V L T E S
318 gagtctcaggaggcagttatggaccgggtgaagttccagagaata
E S Q E A V M D R V K F Q R I
363 tatcaatttgccaagcttaattacaccaagaagccacgtccaat
Y Q F A K L N Y T K E A T S N
408 aaacccaaagctcccgcggtctacgacctggagggtggcagtagc
K P K A P A V Y D L E G G S S
453 aacacgctccttaatttggatcccgaggacgctgtgttttatgtc
N T L L N L D P E D A V F Y V
498 ggaggttaccacccggattttgaacttcctagcagactgcggttc
G G Y P P D F E L P S R L R F
543 cctccatacaaaggctgtatcgaactagatgacctcaatgaaaac
P P Y K G C I E L D D L N E N
588 gttctaagcttgtacaatttcaagacaactttcaatctcaacacc
V L S L Y N F K T T F N L N T
633 acggaggtggagccttgtaggaggagaaaggaagagtcagacaaa
T E V E P C R R R K E E S D K
678 aattactttgaaggtacaggctatgctcgcacccctactcaacca
N Y F E G T G Y A R I P T Q P
723 aatgctcccttcccaaacttcatacagaccatccagactactgtg
N A P F P N F I Q T I Q T T V
768 gacagaggtttactgttcttcgcagaaaaccaggataacttcata
D R G L L F F A E N Q D N F I
813 tctctgaacatagaagatggcaatctcatggtgagatacaaacta
S L N I E D G N L M V R Y K L
858 aattcagagccacccaaagagaagggaattcgagacaccatcaac
N S E P P K E K G I R D T I N
903 gatgggaaagatcattcgatcttaatcacaattggaaaactacaa
D G K D H S I L I T I G K L Q
948 aaacgcatgtggataaatgtgaacgaacgcagtgtacgaatcgaa
K R M W I N V N E R S V R I E
993 ggggaaatattttgatttcagcacatattttgggcggaattcca
G E I F D F S T Y Y L G G I P
1038 attgcaatcagagaaagggtttaacatctcaacgcctgctttccaa
I A I R E R F N I S T P A F Q
1083 ggctgcatgaagaatctgaagaaaaccagtggttggtcaggttg
G C M K N L K K T S G V V R L
1128 aatgatactgtgggtgtaaccaagaagtgtcagaagactggaag
N D T V G V T K K C S E D W K
1173 cttgtgcgaaccgcctcgttctccagaggaggcagatgagcttt

L V R T A S F S R G G Q M S F
1218 acaaacttgagcgtgccctcgactgaccgcttccagctctccttt
T N L D V P S T D R F Q L S F
1263 gggtttcagacctttcaacccagtggcacactgctcaatcatcag
G F Q T F Q P S G T L L N H Q
1308 acgcggaacaagcagcctgctgggtcaccttggaagatgggcacatt
T R T S S L L V T L E D G H I
1353 gagttgagcactagggacagcaacatcccaattttcaagtctcca
E L S T R D S N I P I F K S P
1398 gggacctacatggacgggtttactgcatcatgtatctgtaataagt
G T Y M D G L L H H V S V I S
1443 gacacctcaggtctccgcctttctcatcgatgaccaggtcctgaga
D T S G L R L L I D D Q V L R
1488 aggaaccagaggcttcttagcttctctaacgcccagcagtcgctc
R N Q R L P S F S N A Q Q S L
1533 cgccttgaggaggtcatttccgaggggtgtatcagcaatgtttta
R L G G G H F E G C I S N V L
1578 gtccaaagggttttcacagagtccagaagtcctggatctggccagt
V Q R F S Q S P E V L D L A S
1623 aaatctaccaagaaggatgcatccctaggaggtgcagtttaaac
K S T K K D A S L G G C S L N
1668 aagccaccttttcttatgttgtttaaaagtcccaagagatttaac
K P P F L M L F K S P K R F N
1713 aagggccggattttcaatgttaatcagctgatgcaagatgcacct
A G R I F N V N Q L M Q D A P
1758 caggccacaaggagcacagaggcttggcaagatgggaggtcctgc
Q A T R S T E A W Q D G R S C
1803 ctaccacctctgaacaccaaggcctctcacagagccctgcagttt
L P P L N T K A S H R A L Q F
1848 ggagacagccccaccagccacttgctactcaagcttccccaggaa
G D S P T S H L L L K L P Q E
1893 ctgctgaaacctaggtcacagttttcttttagacatacagacaact
L L K P R S Q F S L D I Q T T
1938 tcccccaaaggactgggtgttttacgcaggcaccaaggactccttc
S P K G L V F Y A G T K D S F
1983 ctggctctttatgtcgcagatggccgtgttgtctttgctttgggg
L A L Y V A D G R V V F A L G
2028 gcaggagggaagaaactgagactcaggagcaaggagagataccat
A G G K K L R L R S K E R Y H
2073 gacgggaagtggcacacgggtggtgttcggactaaatggaggaaag
D G K W H T V V F G L N G G K
2118 gcacgcctgggtgttggtgggttaagggtccaggaaggcagtttg
A R L V V D G L R A Q E G S L
2163 cctggaaattctaccatcagccccagagaacaggtttacctaggg
P G N S T I S P R E Q V Y L G
2208 ttgccgctatcaagaaagccaaagagcctaccccagcacagtttt
L P L S R K P K S L P Q H S F
2253 gtgggggtgcctgagagatttccagttgaactcgaaaccttgat
V G C L R D F Q L N S K P L D
2298 tctccttctgcgaggtttgggttatctccctgcttgggtggctct
S P S A R F G V S P C L G G S
2343 ttagagaaaggcattttatttctcccaaggaggaggccatgtgatc
L E K G I Y F S Q G G G H V I
2388 ctagccaattctgtgtccttggggccagagcttaagctcactttc
L A N S V S L G P E L K L T F

2433 agcattcgcccacggagtcctcactggggtcttaatacacgtcgga
S I R P R S L T G V L I H V G
2478 agtcaatctggacagcgcttaagtgtgtacatggaggcaggaaag
S Q S G Q R L S V Y M E A G K
2523 gtcacaacctctgtgagcagtgatgcaggaggaagtgtgacatca
V T T S V S S D A G G S V T S
2568 attacaccgaagcagtcctctgtgtgatggacagtggcactcggtg
I T P K Q S L C D G Q W H S V
2613 gcagtctccattaaacagcgcatcctgcattctaga 2647
A V S I K Q R I L H L

FIGURE 2

Rattus norvegicus laminin-5 alpha 3 chain
Contains G1 thru G3 subdomains
Cloned as PvuII/XbaI blunt fragment

GAGCTCATTCAGCAGGCCAGAGATGCTGCGAACAAGGTTGCAATTCCCATGAGGTTCAATGG
TAAATCTGGTGTGGAAGTCCGTCTGCCAAATGACCTAGAAGACTTGAAGGGATACACGTCTC
TGTCTTTGTTCCCTCCAAAGACCAGACTTAAGAGAGAATGGAGGCACTGAGGACATGTTTGTA
ATGTACCTTGGAACAAGGATGCCTCCAAGGACTACATCGGCATGGCGGTTGTAGATGGCCA
GCTGACGTGTGTCTACAACCTGGGGGACCGAGAAGCTGAAGTTCAGATCGATCAGGTCCTGA
CGGAGAGTGAGTCTCAGGAGGCAGTTATGGACCGGGTGAAGTTCAGAGAAATATATCAATTT
GCCAAGCTTAATTACACCAAAGAAGCCACGTCCAATAAACCCAAAGCTCCCGCGGTCTACGA
CCTGGAGGGTGGCAGTAGCAACACGCTCCTTAATTTGGATCCCGAGGACGCTGTGTTTTATG
TCGGAGGTTACCCACCGGATTTTGAACCTCCTAGCAGACTGCGGTTCCCTCCATACAAAGGC
TGTATCGAACTAGATGACCTCAATGAAAACGTTCTAAGCTTGTACAATTTCAAGACAACTTT
CAATCTCAACACCACGGAGGTGGAGCCTTGTAGGAGGAGAAAGGAAGAGTCAGACAAAAATT
ACTTTGAAGGTACAGGCTATGCTCGCATCCCTACTCAACCAAATGCTCCCTTCCCAAACCTC
ATACAGACCATCCAGACTACTGTGGACAGAGGTTTACTGTTCTTCGCAGAAAACCAGGATAA
CTTCATATCTCTGAACATAGAAGATGGCAATCTCATGGTGAGATACAACTAAATTCAGAGC
CACCCAAAGAGAAGGGAATTCGAGACACCATCAACGATGGGAAAGATCATTGATCTTAATC
ACAATTGGAAAAC TACAAAAACGCATGTGGATAAATGTGAACGAACGCAGTGTACGAATCGA
AGGGGAAAATATTTGATTT CAGCACATATTATTTGGGCGGAATTCCAATTGCAATCAGAGAAA
GGTTTAAACATCTCAACGCCTGCTTTCCAAGGCTGCATGAAGAATCTGAAGAAAACCAGTGGG
GTTGTCAGGTTGAATGATACTGTGGGTGTAACCAAGAAGTGCTCAGAAGACTGGAAGCTTGT
GCGAACCGCCTCGTTCTCAGAGGAGGGCAGATGAGCTTTACAACTTGGAAGTGCCTCGA
CTGACCGCTTCCAGCTCTCCTTTGGGTTTCAGACCTTTCAACCCAGTGGCACACTGCTCAAT
CATCAGACGCGGACAAGCAGCCTGCTGGTCAACCTGGAAGATGGGCACATTGAGTTGAGCAC
TAGGGACAGCAACATCCCAATTTTCAAGTCTCCAGGGACCTACATGGACGGTTTACTGCATC
ATGTATCTGTAATAAGTGACACCTCAGGTCTCCGCCTTCTCATCGATGACCAGGTCTTGAGA
AGGAACCAGAGGCTTCCTAGCTTCTCTAACGCCAGCAGTCCGCTCCGCCTTGAGAGGAGGTCA
TTTCGAGGGTTGTATCAGCAATGTTTTAGTCCAAAGGTTTTTACAGAGTCCAGAAGTCCTGG
ATCTGGCCAGTAAATCTACCAAGAAGGATGCATCCCTAGGAGGCTGCAGTTTAAACAAGCCA
CCTTTTCTTATGTTGTTTAAAAGTCCCAAGAGATTTAACAAGGGCCGGATTTTCAATGTTAA
TCAGCTG

49 atgaggttcaatggttaaactctggtggtgaagtccgtctgcctaaat
M R F N G K S G V E V R L P N
94 gacctagaagacttgaaggatacacgtctctgtctttgttcctc
D L E D L K G Y T S L S L F L
139 caaagaccagacttaagagagaatggaggcactgaggacatgttt
Q R P D L R E N G G T E D M F
184 gtaatgtaccttgaaacaaggatgcctccaaggactacatcggc
V M Y L G N K D A S K D Y I G
229 atggcggttgtagatggccagctgacgtgtgtctacaacctggg
M A V V D G Q L T C V Y N L G
274 gaccgagaagctgaagttcagatcgatcaggtcctgacggagagt

D R E A E V Q I D Q V L T E S
 319 gagtctcaggaggcagttatggaccgggtgaagttccagagaata
 E S Q E A V M D R V K F Q R I
 364 tatcaatttgccaagcttaattacaccaaagaagccacgtccaat
 Y Q F A K L N Y T K E A T S N
 409 aaacccaaagctcccgcggtctacgacctggagggtggcagtagc
 K P K A P A V Y D L E G G S S
 454 aacacgctccttaatttggatcccgaggacgctgtgttttatgtc
 N T L L N L D P E D A V F Y V
 499 ggagggttaccacccggattttgaacttcctagcagactgcggttc
 G G Y P P D F E L P S R L R F
 544 cctccatacaaaggctgtatcgaactagatgacctcaatgaaaac
 P P Y K G C I E L D D L N E N
 589 gttctaagcttgtacaatttcaagacaactttcaatctcaacacc
 V L S L Y N F K T T F N L N T
 634 acggagggtggagccttgtaggaggagaaaggaagagtcagacaaa
 T E V E P C R R R K E E S D K
 679 aattactttgaagggtacaggctatgctcgcactccctactcaacca
 N Y F E G T G Y A R I P T Q P
 724 aatgctcccttcccaaacttcatacagaccatccagactactgtg
 N A P F P N F I Q T I Q T T V
 769 gacagagggttactgttcttcgcagaaaaccaggataacttcata
 D R G L L F F A E N Q D N F I
 814 tctctgaacatagaagatggcaatctcatggtgagatacaaacta
 S L N I E D G N L M V R Y K L
 859 aattcagagccacccaaagagaagggaattcgagacaccatcaac
 N S E P P K E K G I R D T I N
 904 gatgggaaagatcattcgatcttaatcacaattggaaaactacaa
 D G K D H S I L I T I G K L Q
 949 aaacgcgatgtggataaatgtgaacgaacgcagtgtagaatcgaa
 K R M W I N V N E R S V R I E
 994 ggggaaatatattgatttcagcacatattatttgggcggaattcca
 G E I F D F S T Y Y L G G I P
 1039 attgcaatcagagaaagggtttaacatctcaacgcctgctttccaa
 I A I R E R F N I S T P A F Q
 1084 ggctgcatgaagaatctgaagaaaaccagtggttggtcagggttg
 G C M K N L K K T S G V V R L
 1129 aatgatactgtgggtgtaaccaagaagtgtcagaagactggaag
 N D T V G V T K K C S E D W K
 1174 cttgtgcaaccgcctcgttctccagaggaggcagatgagcttt
 L V R T A S F S R G G Q M S F
 1219 acaaacttggacgtgccctcgactgaccgcttccagctctccttt
 T N L D V P S T D R F Q L S F
 1264 gggtttcagacctttcaacccagtggtcacactgctcaatcatcag
 G F Q T F Q P S G T L L N H Q
 1309 acgcggaacaagcagcctgctggtcaccctggaagatgggcacatt
 T R T S S L L V T L E D G H I
 1354 gagttgagcactaggacagcaacatcccaattttcaagtctcca
 E L S T R D S N I P I F K S P
 1399 gggacctacatggacggttactgcatcatgtatctgtaataagt
 G T Y M D G L L H H V S V I S
 1444 gacacctcaggtctccgccttctcatcgatgaccaggtcctgaga
 D T S G L R L L I D D Q V L R
 1489 aggaaccagagggttcctagcttctctaacgcccagcagtcgctc
 R N Q R L P S F S N A Q Q S L

1534 cgccttggaggaggtcatttcgagggttgtatcagcaatgtttta
R L G G G H F E G C I S N V L
1579 gtccaaagggttttcacagagtcacagaagtcctggatctggccagt
V Q R F S Q S P E V L D L A S
1624 aaatctaccaagaaggatgcatccctaggaggctgcagtttaaac
K S T K K D A S L G G C S L N
1669 aagccaccttttcttatgttggtttaaaagtcccaagagatttaac
K P P F L M L F K S P K R F N
1714 aagggccggattttcaatgttaatcagctg 1743
K G R I F N V N Q L

FIGURE 3

Rattus norvegicus laminin-5 alpha 3 chain
Contains G3 subdomain
Cloned as EcoRI/PvuII blunt fragment

GAATTCCAATTGCAATCAGAGAAAGGTTTAACATCTCAACGCCTGCTTTCCAAGGCTGCATG
AAGAATCTGAAGAAAACCAGTGGGGTTGTCAGGTTGAATGATACTGTGGGTGTAACCAAGAA
GTGCTCAGAAGACTGGAAGCTTGTGCGAACCGCCTCGTTCTCCAGAGGAGGGCAGATGAGCT
TTACAAACTTGACGTGCCCTCGACTGACCGCTTCCAGCTCTCCTTTGGGTTTCAGACCTTT
CAACCCAGTGGCACACTGCTCAATCATCAGACGCGGACAAGCAGCCTGCTGGTCAACCTGGA
AGATGGGCACATTGAGTTGAGCACTAGGGACAGCAACATCCCAATTTTCAAGTCTCCAGGGA
CCTACATGGACGGTTTACTGCATCATGTATCTGTAATAAGTGACACCTCAGGTCTCCGCCTT
CTCATCGATGACCAGGTCCTGAGAAGGAACCAGAGGCTTCCTAGCTTCTCTAACGCCCAGCA
GTCGCTCCGCCTTGGAGGAGGTCATTTTCGAGGGTTGTATCAGCAATGTTTTAGTCCAAAGGT
TTTCACAGAGTCCAGAAGTCCTGGATCTGGCCAGTAAATCTACCAAGAAGGATGCATCCCTA
GGAGGCTGCAGTTTAAACAAGCCACCTTTTCTTATGTTGTTTAAAAGTCCCAAGAGATTTAA
CAAGGGCCGGATTTTCAATGTTAATCAGCTG

60 atgaagaatctgaagaaaaccagtgggggtgtcaggttgaatgat
M K N L K K T S G V V R L N D
105 actgtgggtgtaaccaagaagtgtcagaagactggaagcttgtg
T V G V T K K C S E D W K L V
150 cgaaccgcctcgttctccagaggagggcagatgagctttacaaac
R T A S F S R G G Q M S F T N
195 ttggacgtgccctcgactgaccgcttccagctctcctttgggttt
L D V P S T D R F Q L S F G F
240 cagacctttcaacccagtggcacactgctcaatcatcagacgcgg
Q T F Q P S G T L L N H Q T R
285 acaagcagcctgctgggtcacctggaagatgggcacattgagttg
T S S L L V T L E D G H I E L
330 agcactagggacagcaacatcccaattttcaagtctccagggacc
S T R D S N I P I F K S P G T
375 tacatggacgggtttactgcatcatgtatctgtaataagtacacc
Y M D G L L H H V S V I S D T
420 tcaggtctccgccttctcatcgatgaccaggtcctgagaaggaac
S G L R L L I D D Q V L R R N
465 cagaggcttccctagcttctctaacgcccagcagtcgctccgcctt
Q R L P S F S N A Q Q S L R L
510 ggaggaggtcatttcgaggggtgtatcagcaatgttttagtccaa
G G G H F E G C I S N V L V Q
555 aggttttcacagagtccagaagtcctggatctggccagtaaatct
R F S Q S P E V L D L A S K S
600 accaagaaggatgcacccctaggaggctgcagtttaacaagcca
T K K D A S L G G C S L N K P
645 ccttttcttatgttgttttaaaagtcccaagagatttaacaagggc
P F L M L F K S P K R F N K G
690 cggattttcaatgttaatcagctg 713
R I F N V N Q L

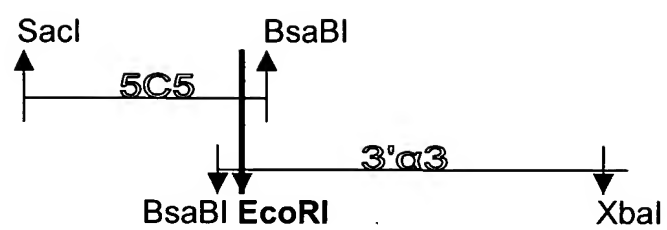


Figure 4

Figure 5

Table 1. Cloning and expression vectors constructed for rat laminin 5-alpha 3 chain G Domains

<u>Name</u>	<u>vector</u>	<u>transformed</u>	<u>insert</u>	<u>cloning region</u>	<u>restriction digest</u>	<u>designed from</u>
pHB1	pGEM T-easy	<i>E. coli</i> GM2163	5C5	932-3242 bp	designed PCR primers	original cDNA fragment
pHB2	pGEM T-easy	<i>E. coli</i> GM2163	3'alpha3	3092-5250 bp	designed PCR primers	original cDNA fragment
pHB3	pYES2	<i>E. coli</i> DH5alphaMCR	modified 3'alpha3	1761 bp fragment	XbaI/ EcoRI partial	pHB2
pHB4	pYES2	<i>E. coli</i> DH5alphaMCR	G1-G5	822 bp fragment	SacI/ EcoRI	pHB1
pHB5	does not exist		modified 5C5	added to 3'alpha3 in vector	SacI/ EcoRI	pHB3
pHB6	pPICZalphaB	<i>P. pastoris</i> SMD1168	G1-G5	2364-4990 bp	SacI'/ XbaI	pHB4
pHB7	pPICZalphaB	<i>P. pastoris</i> SMD1168	G3-G5	3239-4990 bp	EcoRI/ XbaI	pHB6
pHB8	pPICZalphaB	<i>P. pastoris</i> SMD1168	G1-G3	2364-4097 bp	PvuII/ XbaI'	pHB6
pHB9	pPICZalphaB	<i>P. pastoris</i> SMD1168	G3	3386-4097 bp	EcoRI/ PvuII'	pHB7

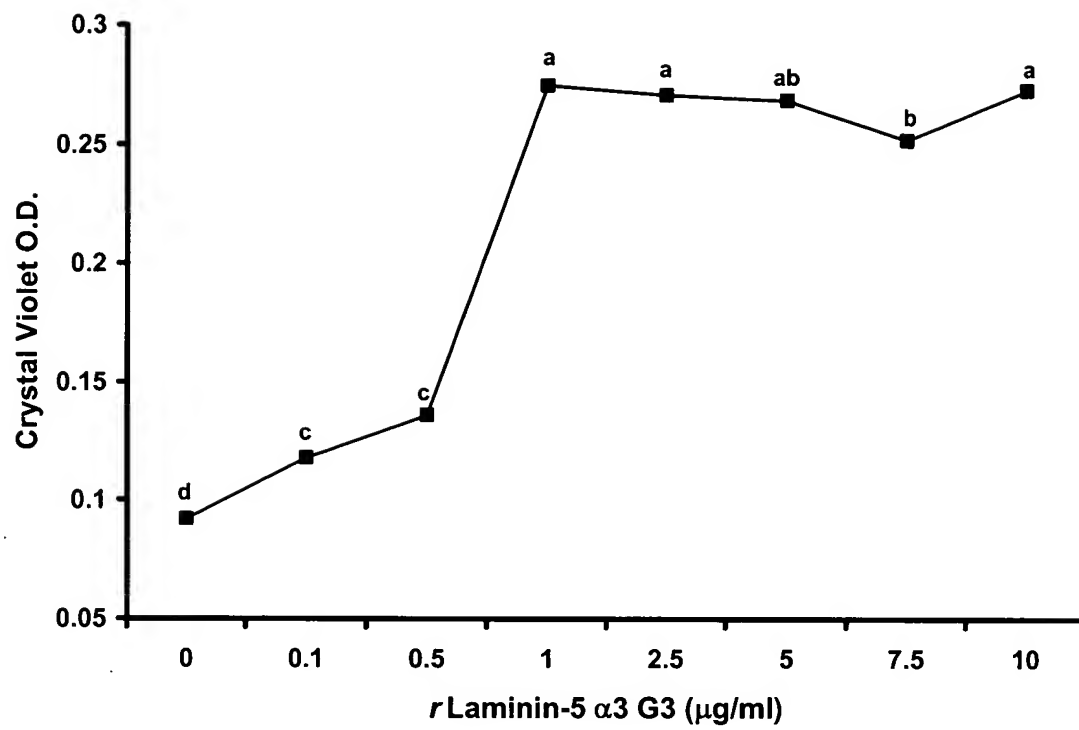


Figure 6

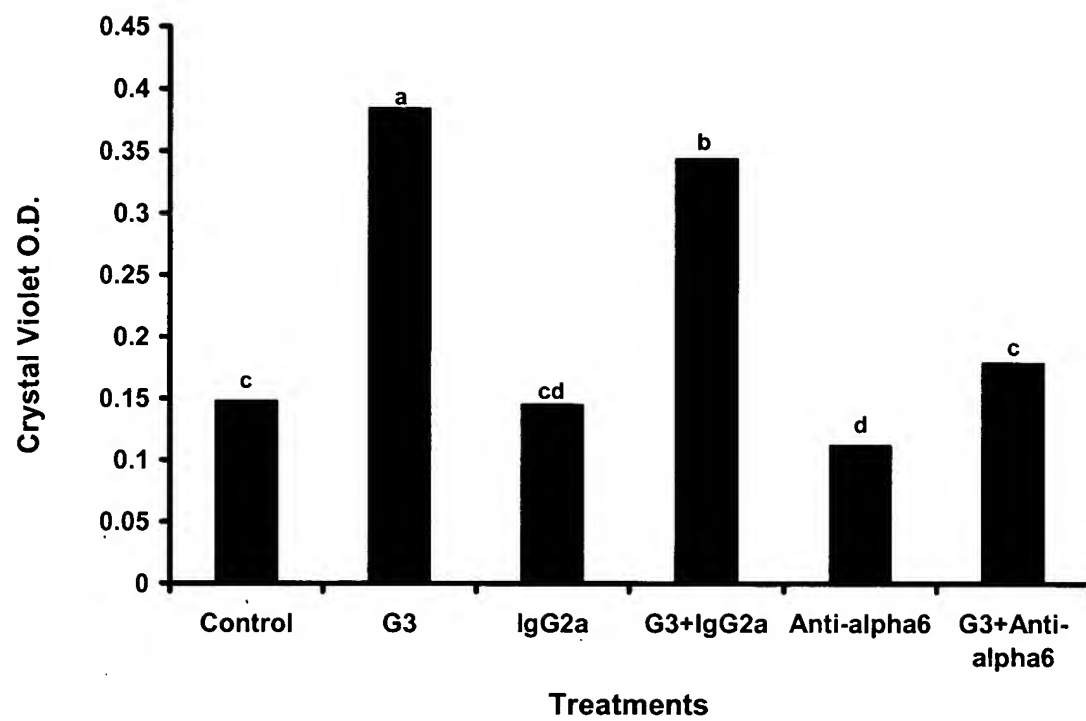


Figure 7

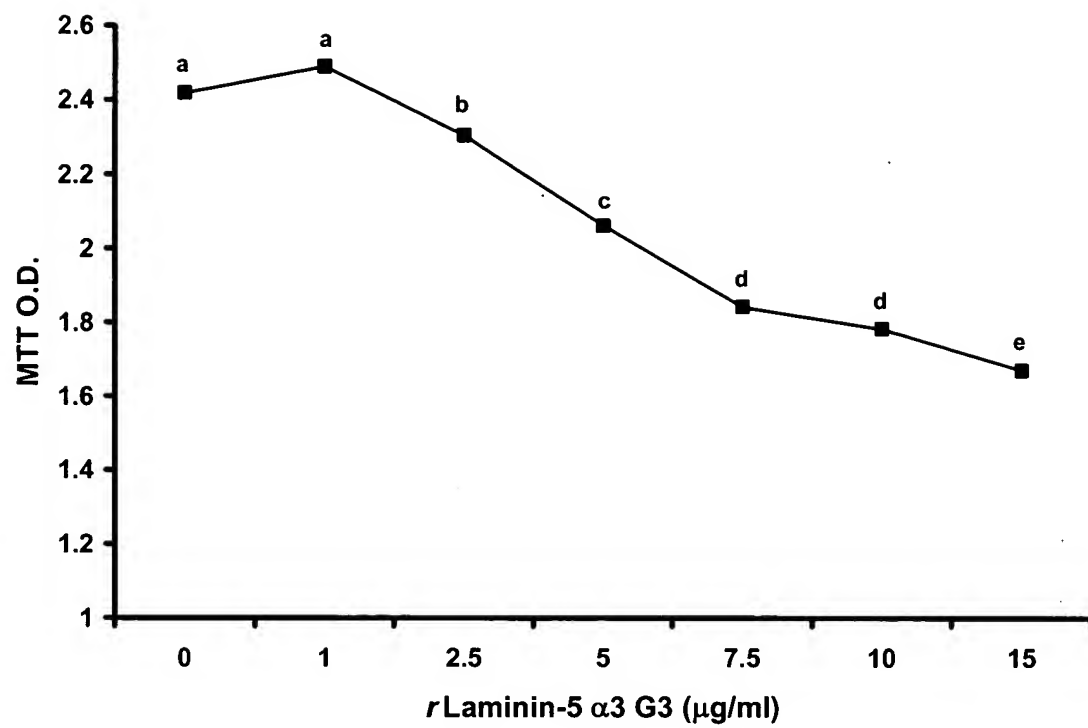


Figure 8

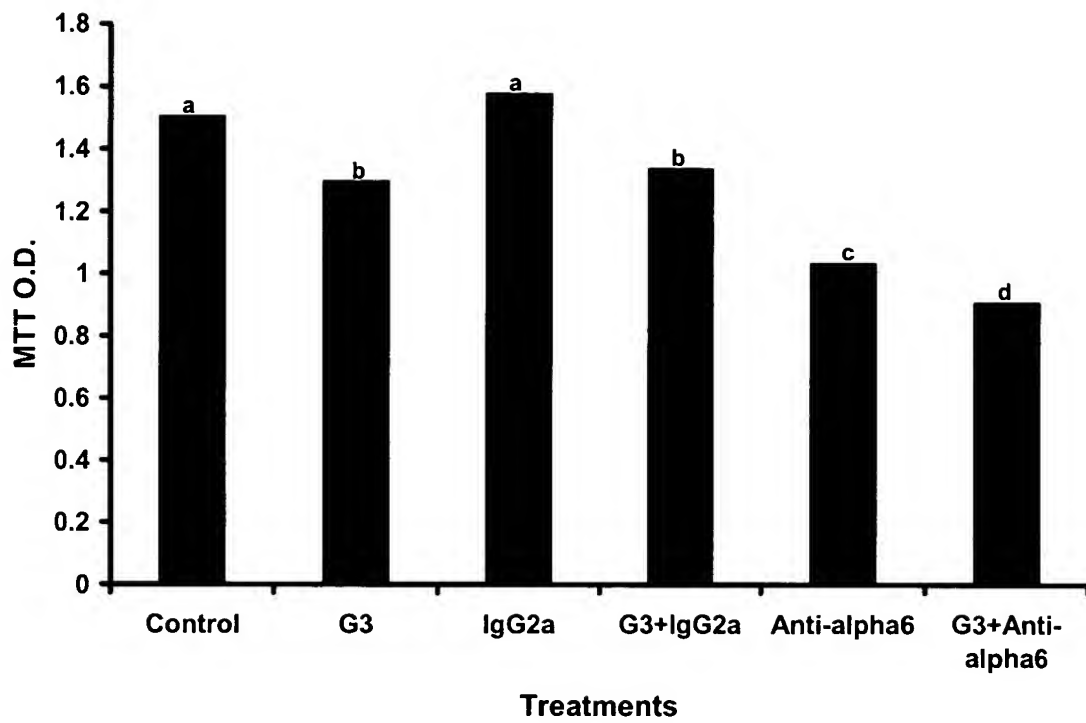


Figure 9